

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/698,341

DATE: 02/27/2001  
 TIME: 15:27:52

Input Set : A:\sequencelist.txt  
 Output Set: N:\CRF3\02272001\I698341.raw

3 <110> APPLICANT: Sorge, Joseph  
 4 Hurlbut Hogrefe, Holly  
 5 Connie, Hansen  
 7 <120> TITLE OF INVENTION: Compositions and Methods Utilizing DNA Polymerases  
 9 <130> FILE REFERENCE: 25436/1560  
 11 <140> CURRENT APPLICATION NUMBER: 09/698,341  
 12 <141> CURRENT FILING DATE: 2000-10-27  
 14 <150> PRIOR APPLICATION NUMBER: 60/162,600  
 15 <151> PRIOR FILING DATE: 1999-10-29  
 17 <160> NUMBER OF SEQ ID NOS: 48  
 19 <170> SOFTWARE: PatentIn version 3.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 2331  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Thermococcus sp. JDF-3  
 26 <400> SEQUENCE: 1  
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 29 aaggagaaag gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg 120  
 31 ctctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc 180  
 33 agggtcgtta aggttaagcg cgcggagaag gtgaagaaaa agttctcgg caggctctgtg 240  
 35 gaggtctggg tctctactt cagcaccccg caggacgttc cggcaatccg cgacaaaata 300  
 37 aggaagcacc ccgcggtcat cgacatctac gagtacgaca tacccttcgc caagcgtac 360  
 39 ctcatagaca agggcctaata cccgatggaa ggtgaggaa agcttaaaact catgtctctc 420  
 41 gacatcgaga cgtctacca cgaggagaa gagtttgaa ccgggccgat tctgatgata 480  
 43 agctaagccg atgaaagcga ggcgcgcgtg ataacctgga agaagatcga ccttccttac 540  
 45 gttgaggttg tctccaccga gaaggagatg attaagcgt tcttgagggt cgttaaggag 600  
 47 aaggaccgag acgtgctgat aacatacaac ggcgacaact tcgacttcgc ctacctgaaa 660  
 49 aagcgtctgt agaagcttgg cgtgagcttt accctcgga gggacgggag cgaagcgaag 720  
 51 atacagcgca tgggggacag gtttgcggtc gaggtgaagg gcagggtaca ctteagacct 780  
 53 tatccagtca taaggcgac cataaacctc ccgacctaca cccttgaggc tgtatacgag 840  
 55 gcgggttttc gcaagcccaa ggagaaggtc tacgcccagg agatagccac cgcctgggag 900  
 57 accggcgagg ggccttgagg ggtcgcgcgc tactcgatgg aggaacgcgag ggttacctac 960  
 59 gacgttgga gggagttctt cccgatggag gccagcttt ccaggctcat cggccaagyc 1020  
 61 ctctgggagc ttcccgctc cagcaccgyc aacctcgtc agtggttct cctaaggaaag 1080  
 63 gcctacgaga ggaacgaact cgtcccaac aagcccgac agagggagct ggcgaggaga 1140  
 65 agggggggct acgccggtg ctacgtcaag gacccggagc ggggactgtg ggacaatac 1200  
 67 gtgtatctag actttcgtg tctctacct tcaatcataa tcaaccacaa cgtctcgcca 1260  
 69 gatacgtca accgcgagg gtgtaggagc tacgacgttg ccccgaggc cgttcacaag 1320  
 71 ttctgcaagg acttcccggt cttcattccg agcctgctc gaaacctgct ggaggaaag 1380  
 73 cagaagataa agaggagat gaaggcaact ctgcaccgc lggagaagaa tctctctgat 1440  
 75 tacaggcaac gcgccatcaa gatctcgcgc aacagctact acggctacta cggctatgcc 1500  
 77 agggcaagat ggtactgcag gtagtgcgcc gagagcgtta cggcatgggg aaggaggtac 1560  
 79 atcgaaatgg tcalcagaga gcttgaggaa aagttcggt ttaaagtcct ctatgcagac 1620  
 81 acagacggtc tccatgccac cattcctgga cgggacgctg aaacagtcaa gaaaaaggca 1680  
 83 atggagttct taaactatat caatcccaaa ctgcccggcc ttctcgaact cgaatacgag 1740  
 85 ggcttctacg tcaggggctt cttcgtcacg aagaaaaagt acgcggtcat cgacgaggag 1800  
 87 ggcaagataa ccacgcgcg gcttgagata gtcaggcgcg actggagcga gatagcgaag 1860

ENTERED

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89 gagacgcagg cgagggtttt ggaggcgata ctcaggcacg gtgacgttga agaggccgtc 1920
91 agaattgtca ggaaggtcac cgaagagctg agcaagtacg aggttccgcc ggagaagctg 1980
93 gttatccacg agcagataac gcgcgagctc aaggactaca aggccaccgg cccgcacgta 2040
95 gccatagcga agcgtttggc cgcagagagt gttaaaatcc ggcgcggaac tgtgataagc 2100
97 tacatcgttc tgaagggttc cgggaaggata ggcgacaggg cgattccctt cgacgagttc 2160
99 gacccgacga agcacaagta cgatgcggac tactacatcg agaaccaggt tctgcccga 2220
101 gttgagagaa tcttcagggc cttcggttac cgcaagggaag acctgcgcta ccagaagacy 2280
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107 <211> LENGTH: 776
108 <212> TYPE: PRT
109 <213> ORGANISM: Thermococcus sp. JDF-3
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116 Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
117 20 25 30
119 Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
120 35 40 45
122 Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
123 50 55 60
125 Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
126 65 70 75 80
128 Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
129 85 90 95
131 Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
132 100 105 110
134 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
135 115 120 125
137 Met Glu Gly Glu Glu Glu Lys Leu Met Ser Phe Asp Ile Glu Thr
138 130 135 140
140 Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
141 145 150 155 160
143 Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile
144 165 170 175
146 Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys
147 180 185 190
149 Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr
150 195 200 205
152 Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu
153 210 215 220
155 Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys
156 225 230 235 240
158 Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val
159 245 250 255
161 His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
162 260 265 270
164 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu
165 275 280 285

```

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TECH CENTER 1600/2900

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167 Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly
168      290      295      300
170 Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr
171 305      310      315      320
173 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
174      325      330      335
176 Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
177      340      345      350
179 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
180      355      360      365
182 Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr
183      370      375      380
185 Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile
186 385      390      395      400
188 Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
189      405      410      415
191 Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp
192      420      425      430
194 Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
195      435      440      445
197 Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys
198      450      455      460
200 Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp
201 465      470      475      480
203 Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr
204      485      490      495
206 Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser
207      500      505      510
209 Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu
210      515      520      525
212 Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu
213      530      535      540
215 His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala
216 545      550      555      560
218 Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu
219      565      570      575
221 Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys
222      580      585      590
224 Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu
225      595      600      605
227 Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
228      610      615      620
230 Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val
231 625      630      635      640
233 Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro
234      645      650      655
236 Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp
237      660      665      670
239 Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala

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240          675          680          685
242 Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu
243          690          695          700
245 Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
246 705          710          715          720
248 Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln
249          725          730          735
251 Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
252          740          745          750
254 Glu Asp Leu Arg Tyr Gln Lys Thr Arg Glu Val Gly Leu Gly Ala Trp
255          755          760          765
257 Leu Lys Pro Lys Gly Lys Lys
258          770          775
260 <210> SEQ ID NO: 3
261 <211> LENGTH: 1300
262 <212> TYPE: PRT
263 <213> ORGANISM: Thermococcus sp. JDF-3
265 <220> FEATURE:
266 <221> NAME/KEY: UNSURE
267 <222> LOCATION: (1015)..(1015)
268 <223> OTHER INFORMATION: X = unknown
271 <400> SEQUENCE: 3
273 Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
274 1          5          10          15
276 Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
277          20          25          30
279 Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
280          35          40          45
282 Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
283          50          55          60
285 Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
286 65          70          75          80
288 Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
289          85          90          95
291 Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
292          100          105          110
294 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
295          115          120          125
297 Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
298          130          135          140
300 Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
301 145          150          155          160
303 Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile
304          165          170          175
306 Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys
307          180          185          190
309 Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr
310          195          200          205
312 Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu

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313      210      215      220
315 Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys
316 225      230      235      240
318 Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val
319      245      250      255
321 His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
322      260      265      270
324 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu
325      275      280      285
327 Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly
328      290      295      300
330 Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr
331 305      310      315      320
333 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
334      325      330      335
336 Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
337      340      345      350
339 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
340      355      360      365
342 Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr
343      370      375      380
345 Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile
346 385      390      395      400
348 Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
349      405      410      415
351 Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp
352      420      425      430
354 Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
355      435      440      445
357 Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys
358      450      455      460
360 Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp
361 465      470      475      480
363 Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Leu Leu Pro Gly
364      485      490      495
366 Glu Trp Val Ala Val Ile Glu Gly Gly Lys Leu Arg Pro Val Arg Ile
367      500      505      510
369 Gly Glu Leu Val Asp Gly Leu Met Glu Ala Ser Gly Glu Arg Val Lys
370      515      520      525
372 Arg Asp Gly Asp Thr Glu Val Leu Glu Val Glu Gly Leu Tyr Ala Ser
373      530      535      540
375 Pro Ser Thr Gly Ser Pro Arg Lys Pro Ala Gln Cys Arg Lys Pro Gly
376 545      550      555      560
378 Thr Ala Met Pro Gly Lys Phe Thr Glu Leu Ser Thr Pro Glu Gly Gly
379      565      570      575
381 Leu Ser Val Thr Arg Gly His Ser Leu Phe Ala Tyr Arg Asp Ala Ser
382      580      585      590
384 Leu Trp Arg Arg Gly Arg Arg Arg Phe Lys Pro Gly Asp Leu Leu Ala
385      595      600      605

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
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Input Set : A:\sequencelist.txt  
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L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:970 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:1146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:1380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32  
L:1420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:1739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40